

**Research Activity Report**  
**Supported by “Leading Graduate Program in Primatology and Wildlife Science”**  
 (Please be sure to submit this report after the trip that supported by PWS.)

|                             |                               |
|-----------------------------|-------------------------------|
| 2016. 06, 16                |                               |
| <b>Affiliation/Position</b> | Primate Research Institute/M1 |
| <b>Name</b>                 | Kota Kuroki                   |

**1. Country/location of visit**

Kyoto-city, Kyoto Pref., Japan

**2. Research project**

Genome science course

**3. Date (departing from/returning to Japan)**

2016. 05. 30 – 2016. 06. 03 (5days)

**4. Main host researcher and affiliation**

Primatology and Wildlife Science Leading Graduate Program, Kyoto University

**5. Progress and results of your research/activity** (You can attach extra pages if needed)

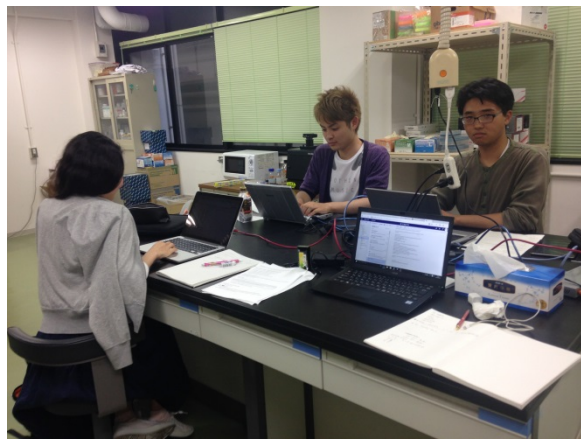
Please insert one or more pictures (to be publicly released). Below each picture, please provide a brief description.

In this course, the participants were divided into 3 groups, whole-genome, deer, and fig/insects group. I belonged to whole-genome group. In this group, we analyzed the whole-genome of the Japanese macaque in Yakushima (*Macaca fuscata yakui*; Yakuzaru).

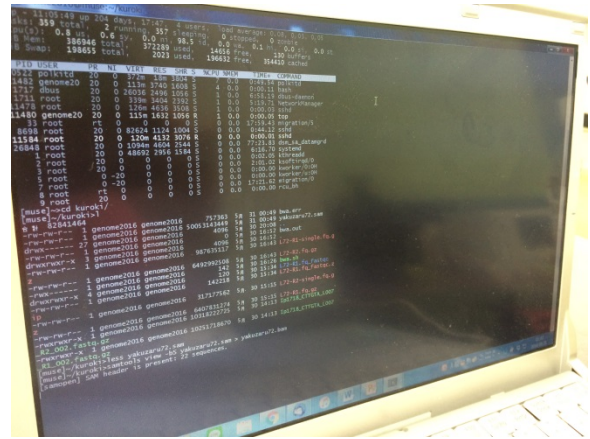
We mainly analyzed two things;  
 1, Yakuzarus’ population history by PSMC analysis  
 2, variants of base sequence on genes  
 In this analysis, we used rhesus monkey’s (*Macaca mulatta*) DNA as reference genome.

By PSMC analysis, we graphed the population history of Yakuzaru until about 1 million years ago. And we identified the divergence period of Yakuzaru and rhesus macaque.

Also, we confirmed that ZNF37A gene has 11 stop codons in Yakuzaru by gene variants analysis. This gene is known to involving in myogenesis.



Analyzing  
Photo by Kei Hazehara



The display of Cigwin which is used for analyzing

**6. Others**

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